

SEQUENCE LISTING

<110> Jackson, W. James
Pace, John

<120> Chlamydia Protein, Gene Sequence and Uses Thereof

<130> 7969-062-999

<140> 08/942,596

<141> 1997-10-02

<160> 43

<170> PatentIn version 3.0

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<211> 4435

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Recombinant Expression Vector

<220>

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ttttagcctg caaatagtgt aattattgga tcctgtaaag agaaaaggac gaatgcgctg	300
aagataagaa catttattga tattaataa ttaatttttt atgaagcggg gtaattaatt	360
ttatctctca gcttttgtgt g atg caa acg tct ttc cat aag ttc ttt ctt	411
Met Gln Thr Ser Phe His Lys Phe Phe Leu	
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tca atg att cta gct tat tct tgc tgc tct tta aat ggg ggg gga tat	459
Ser Met Ile Leu Ala Tyr Ser Cys Cys Ser Leu Asn Gly Gly Gly Tyr	
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gca gca gaa atc atg gtt cct caa gga att tac gat ggg gag acg tta	507
Ala Ala Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu	
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act gta tca ttt ccc tat act gtt ata gga gat ccg agt ggg act act	555
Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr	
45 50 55	
ggt ttt tct gca gga gag tta aca tta aaa aat ctt gac aat tct att	603
Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile	
60 65 70	
gca gct ttg cct tta agt tgt ttt ggg aac tta tta ggg agt ttt act	651
Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr	
75 80 85 90	
ggt tta ggg aga gga cac tcg ttg act ttc gag aac ata cgg act tct	699
Val Leu Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser	
95 100 105	
aca aat ggg gca gct cta agt aat agc gct gct gat gga ctg ttt act	747
Thr Asn Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr	
110 115 120	

att gag ggt ttt aaa gaa tta tcc ttt tcc aat tgc aat tca tta ctt	795
Ile Glu Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu	
125 130 135	
gcc gta ctg cct gct gca acg act aat aag ggt agc cag act ccg acg	843
Ala Val Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr	
140 145 150	
aca aca tct aca ccg tct aat ggt act att tat tct aaa aca gat ctt	891
Thr Thr Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu	
155 160 165 170	
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Leu Leu Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser	
175 180 185	
gga gat ggg gga gct ata gat gct aag agc tta acg gtt caa gga att	987
Gly Asp Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile	
190 195 200	
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Ser Lys Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly	
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Ala Cys Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro	
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Ile Ala Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly Ile Ala	
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Asp Pro Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly	
270 275 280	
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Phe Leu Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro	
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Val Tyr Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr	
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Gln Ala Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly	
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Val Val Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile	
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Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu	
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Arg Asn Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly	
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Glu Leu Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn	
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Leu Lys Arg Thr Ala Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr	
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Val Ser Ser Ser Gln Ala Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr	
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Leu Arg Ala Lys Ala Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu	
460 465 470	
atg gca aac gga aat aac cag cca gcg cag tct tcc aaa ctt cta aaa	1851
Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys	
475 480 485 490	
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Ile Asn Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly	
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Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val	
510 515 520	
ctt cgt gaa aag gca aaa tta tca gtg aat tct cta agt cag aca ggt	1995
Leu Arg Glu Lys Ala Lys Leu Ser Val Asn Ser Leu Ser Gln Thr Gly	
525 530 535	
ggg agt ctg tat atg gaa gct ggg agt aca tgg gat ttt gta act cca	2043
Gly Ser Leu Tyr Met Glu Ala Gly Ser Thr Trp Asp Phe Val Thr Pro	
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Gln Pro Pro Gln Gln Pro Pro Ala Ala Asn Gln Leu Ile Thr Leu Ser	
555 560 565 570	
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Asn Leu His Leu Ser Leu Ser Ser Leu Leu Ala Asn Asn Ala Val Thr	
575 580 585	
aat cct cct acc aat cct cca gcg caa gat tct cat cct gca gtc att	2187
Asn Pro Pro Thr Asn Pro Pro Ala Gln Asp Ser His Pro Ala Val Ile	
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Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile Phe Phe	
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Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser	
620 625 630	
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Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly Thr Lys Pro Pro	
635 640 645 650	
gct aat gcc cca tca gat ttg act cta ggg aat gag atg cct aag tat	2379
Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu Met Pro Lys Tyr	
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ggc tat caa gga agc tgg aag ctt gcg tgg gat cct aat aca gca aat	2427
Gly Tyr Gln Gly Ser Trp Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn	
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Asp Gly Arg Ser Tyr Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn	
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Phe Phe Tyr His Asp Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile	
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Ser Gly Gly Tyr Ser Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met	
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Val Cys Arg Ser Asn His His Ala Cys Ile Gly Ser Val Tyr Leu Ser	
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acc caa caa gct tta tgt gga tcc tat ttg ttc gga gat gcg ttt atc	2859
Thr Gln Gln Ala Leu Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile	
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cgt gct agc tac ggg ttt ggg aat cag cat atg aaa acc tca tat aca	2907
Arg Ala Ser Tyr Gly Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr	
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Phe Ala Glu Ser Asp Val Arg Trp Asp Asn Asn Cys Leu Ala Gly	
845 850 855	
gag att gga gcg gga tta ccg att gtg att act cca tct aag ctc tat	3003
Glu Ile Gly Ala Gly Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr	
860 865 870	
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cat gaa tct ttt aca gag gaa ggc gat caa gct cgg gca ttc aag agc	3099
His Glu Ser Phe Thr Glu Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser	
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gga cat ctc cta aat cta tca gtt cct gtt gga gtg aag ttt gat cga	3147
Gly His Leu Leu Asn Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg	
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tgt tct agt aca cat cct aat aaa tat agc ttt atg gcg gct tat atc	3195
Cys Ser Ser Thr His Pro Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile	
925 930 935	
tgt gat gct tat cgc acc atc tct ggt act gag aca acg ctc cta tcc	3243
Cys Asp Ala Tyr Arg Thr Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser	
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cat caa gag aca tgg aca aca gat gcc ttt cat tta gca aga cat gga	3291
His Gln Glu Thr Trp Thr Thr Asp Ala Phe His Leu Ala Arg His Gly	
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gta tat ggc cat gga aga tat gag tat cga gat gct tct cga ggc tat	3387
Val Tyr Gly His Gly Arg Tyr Glu Tyr Arg Asp Ala Ser Arg Gly Tyr	
990 995 1000	
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Gly Leu Ser Ala Gly Ser Arg Val Arg Phe	
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Gln	Pro	Ala	Gln	Ser	Lys	Leu	Leu	Lys	Ile	Asn	Asp	Gly	Glu	Gly			
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Ala	Ser	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Ile	Leu	Asp	Ile	Arg		
705					710				715						720		
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Pro	Ile	Val	Ile	Thr	Pro	Ser	Lys	Leu	Tyr	Leu	Asn	Glu	Leu	Arg	Pro		
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 Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile Cys Asp Ala Tyr Arg Thr
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 Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser His Gln Glu Thr Trp Thr
 945 950 955 960
 Thr Asp Ala Phe His Leu Ala Arg His Gly Val Val Val Arg Gly Ser
 965 970 975
 Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly Arg
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 Ser Phe Xaa Tyr
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 aatccttgaca attctattgc agctttgcct ttaagttgtt ttgggaactt attagggagt 180
 tttactgttt tagggagagg acactcgttg actttcgaga acatacggac ttctacaaat 240
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ggatccaata	actctggatc	agtttccctt	gatggagagg	gagtagtttt	ctttagtagc	1020
aatgtagctg	ctgggaaagg	gggagctatt	tatgccaaaa	agctctcggg	tgctaactgt	1080
ggccctgtac	aattttttaag	gaatatcgct	aatgatgggt	gagcgattta	tttaggagaa	1140
tctggagagc	tcagttttatc	tgctgattat	ggagatatta	ttttcgatgg	gaatcttaaa	1200
agaacagcca	aagagaatgc	tgccgaatgt	aatggcgtaa	ctgtgtcctc	acaagccatt	1260
tcgatgggat	cgggagggaa	aataacgaca	ttaagagcta	aagcagggca	tcagattctc	1320
tttaatgatc	ccatcgagat	ggcaaacgga	aataaccagc	cagcgagtc	ttccaaactt	1380
ctaaaaatta	acgatgggtga	aggatacaca	ggggatattg	tttttgctaa	tggaagcagt	1440
actttgtacc	aaaatgttac	gatagagcaa	ggaaggattg	ttcttcgtga	aaaggcaaaa	1500
ttatcagtga	a					1511

<210> 11
 <211> 1444
 <212> DNA
 <213> Chlamydia sp.

<400> 11	
ttctctaagt	cagacaggtg
aactccacaa	ccaccacaac
gcatttgtct	ctttcttctt
tccagcgcaa	gattctcatc
tagtgggcct	atcttttttg
aggttcta	caaaaaatca
tgccccatca	gatttgactc
gaagcttgcg	tggtatccta
gactaaaact	gggtataatc
atggggatcc	attttagata
gcgctcttat	tgctcaggat
cgatgcttta	ggtcagggat
ctactttgga	tcacgatagt
ttatgtatgt	tgctgttcca
acaagcttta	tggtggatcct
tggaatcag	catatgaaaa
taataactgt	ctggctggag
gctctatttg	aatgagttgc
atctttttaca	gaggaaggcg
atcagttcct	gttggagtga
ctttatggcg	gcttatatct
cctatcccat	caagagacat
ggtttagagga	tctatgtatg
atatgagtat	cgagatgctt
ctaa	

<210> 12
 <211> 56
 <212> DNA
 <213> Chlamydia sp.

<400> 12	
aagggcccaa	ttacgcagag
ggtaccgaaa	ttatggttcc
tcaaggaatt	tacgat

<210> 13
 <211> 56
 <212> DNA
 <213> Chlamydia sp.

<400> 13
aagggcccaa ttacgcagag ggtaccctaa gaagaaggca tgccgtgcta gcggag 56

<210> 14
<211> 57
<212> DNA
<213> Chlamydia sp.

<400> 14
aagggcccaa ttacgcagag ggtaccggag agctcgcgaa tccatacgaa taggaac 57

<210> 15
<211> 1013
<212> PRT
<213> Chlamydia sp.

<400> 15
Met Gln Thr Ser Phe His Lys Phe Phe Leu Ser Met Ile Leu Ala Tyr
1 5 10 15
Ser Cys Cys Ser Leu Asn Gly Gly Gly Tyr Ala Ala Glu Ile Met Val
20 25 30
Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr
35 40 45
Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu
50 55 60
Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser
65 70 75 80
Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His
85 90 95
Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu
100 105 110
Ser Asp Ser Ala Asn Ser Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu
115 120 125
Leu Ser Phe Ser Asn Cys Asn Pro Leu Leu Ala Val Leu Pro Ala Ala
130 135 140
Thr Thr Asn Asn Gly Ser Gln Thr Pro Ser Thr Thr Ser Thr Pro Ser
145 150 155 160
Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Leu Asn Asn Glu
165 170 175
Lys Phe Ser Phe Tyr Ser Asn Ser Val Ser Gly Asp Gly Gly Ala Ile
180 185 190
Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys Val Phe
195 200 205
Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr
210 215 220
Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Val Ala Asn
225 230 235 240
Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val Gln Asp Gly Gln
245 250 255
Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro Val Val Ser Phe
260 265 270
Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val Ala Arg Val Gly
275 280 285
Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn Gly Lys
290 295 300
Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr Ile Ala Ala Glu
305 310 315 320
Gln Pro Thr Asn Gly Gln Ala Ser Asn Thr Ser Asp Asn Tyr Gly Asp
325 330 335
Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala Ala Gly Ser Asn
340 345 350

Asn	Ser	Gly	Ser	Val	Ser	Phe	Asp	Gly	Glu	Gly	Val	Val	Phe	Phe	Ser
		355					360					365			
Ser	Asn	Val	Ala	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ala	Lys	Lys	Leu
		370				375					380				
Ser	Val	Ala	Asn	Cys	Gly	Pro	Val	Gln	Leu	Leu	Gly	Asn	Ile	Ala	Asn
385					390					395					400
Asp	Gly	Gly	Ala	Ile	Tyr	Leu	Gly	Glu	Ser	Gly	Glu	Leu	Ser	Leu	Ser
			405					410						415	
Ala	Asp	Tyr	Gly	Asp	Met	Ile	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Thr	Ala
			420					425						430	
Lys	Glu	Asn	Ala	Ala	Asp	Val	Asn	Gly	Val	Thr	Val	Ser	Ser	Gln	Ala
		435					440					445			
Ile	Ser	Met	Gly	Ser	Gly	Gly	Lys	Ile	Thr	Thr	Leu	Arg	Ala	Lys	Ala
		450				455					460				
Gly	His	Gln	Ile	Leu	Phe	Asn	Asp	Pro	Ile	Glu	Met	Ala	Asn	Gly	Asn
465					470					475					480
Asn	Gln	Pro	Ala	Gln	Ser	Ser	Glu	Pro	Leu	Lys	Ile	Asn	Asp	Gly	Glu
				485					490					495	
Gly	Tyr	Thr	Gly	Asp	Ile	Val	Phe	Ala	Asn	Gly	Asn	Ser	Thr	Leu	Tyr
			500					505					510		
Gln	Asn	Val	Thr	Ile	Glu	Gln	Gly	Arg	Ile	Val	Leu	Arg	Glu	Lys	Ala
		515					520					525			
Lys	Leu	Ser	Val	Asn	Ser	Leu	Ser	Gln	Thr	Gly	Gly	Ser	Leu	Tyr	Met
		530				535					540				
Glu	Ala	Gly	Ser	Thr	Leu	Asp	Phe	Val	Thr	Pro	Gln	Pro	Pro	Gln	Gln
545					550					555					560
Pro	Pro	Ala	Ala	Asn	Gln	Ser	Ile	Thr	Leu	Ser	Asn	Leu	His	Leu	Ser
				565					570					575	
Leu	Ser	Ser	Leu	Leu	Ala	Asn	Asn	Ala	Val	Thr	Asn	Pro	Pro	Thr	Asn
			580					585					590		
Pro	Pro	Ala	Gln	Asp	Ser	His	Pro	Ala	Val	Ile	Gly	Ser	Thr	Thr	Ala
		595					600					605			
Gly	Ser	Val	Thr	Ile	Ser	Gly	Pro	Ile	Phe	Phe	Glu	Asp	Leu	Asp	Asp
		610				615					620				
Thr	Ala	Tyr	Asp	Arg	Tyr	Asp	Trp	Leu	Gly	Ser	Asn	Gln	Lys	Ile	Asp
625					630					635					640
Val	Leu	Lys	Leu	Gln	Leu	Gly	Thr	Gln	Pro	Pro	Ala	Asn	Ala	Pro	Ser
				645					650					655	
Asp	Leu	Thr	Leu	Gly	Asn	Glu	Met	Pro	Lys	Tyr	Gly	Tyr	Gln	Gly	Ser
			660					665					670		
Trp	Lys	Leu	Ala	Trp	Asp	Pro	Asn	Thr	Ala	Asn	Asn	Gly	Pro	Tyr	Thr
		675					680					685			
Leu	Lys	Ala	Thr	Trp	Thr	Lys	Thr	Gly	Tyr	Asn	Pro	Gly	Pro	Glu	Arg
		690				695					700				
Val	Ala	Ser	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Ile	Leu	Asp	Ile
705					710					715					720
Arg	Ser	Ala	His	Ser	Ala	Ile	Gln	Ala	Ser	Val	Asp	Gly	Arg	Ser	Tyr
				725					730					735	
Cys	Arg	Gly	Leu	Trp	Val	Ser	Gly	Val	Ser	Asn	Phe	Phe	Tyr	His	Asp
			740					745					750		
Arg	Asp	Ala	Leu	Gly	Gln	Gly	Tyr	Arg	Tyr	Ile	Ser	Gly	Gly	Tyr	Ser
		755					760					765			
Leu	Gly	Ala	Asn	Ser	Tyr	Phe	Gly	Ser	Ser	Met	Phe	Gly	Leu	Ala	Phe
		770				775					780				
Thr	Glu	Val	Phe	Gly	Arg	Ser	Lys	Asp	Tyr	Val	Val	Cys	Arg	Ser	Asn
785					790					795					800
His	His	Ala	Cys	Ile	Gly	Ser	Val	Tyr	Leu	Ser	Thr	Lys	Gln	Ala	Leu
				805					810					815	
Cys	Gly	Ser	Tyr	Val	Phe	Gly	Asp	Ala	Phe	Ile	Arg	Ala	Ser	Tyr	Gly
			820					825					830		
Phe	Gly	Asn	Gln	His	Met	Lys	Thr	Ser	Tyr	Thr	Phe	Ala	Glu	Glu	Ser
		835					840						845		

Asp Val Cys Trp Asp Asn Asn Cys Leu Val Gly Glu Ile Gly Val Gly
 850 855 860
 Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg
 865 870 875 880
 Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr
 885 890 895
 Glu Glu Gly Asp Gln Ala Arg Ala Phe Arg Ser Gly His Leu Met Asn
 900 905 910
 Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His
 915 920 925
 Pro Asn Lys Tyr Ser Phe Met Gly Ala Tyr Ile Cys Asp Ala Tyr Arg
 930 935 940
 Thr Ile Ser Gly Thr Gln Thr Thr Leu Leu Ser His Gln Glu Thr Trp
 945 950 955 960
 Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Ile Val Arg Gly
 965 970 975
 Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly
 980 985 990
 Arg Tyr Glu Tyr Arg Asp Thr Ser Arg Gly Tyr Gly Leu Ser Ala Gly
 995 1000 1005
 Ser Lys Val Arg Phe
 1010

<210> 16
 <211> 1013
 <212> PRT
 <213> Chlamydia sp.

<400> 16
 Met Gln Thr Ser Phe His Lys Phe Phe Leu Ser Met Ile Leu Ala Tyr
 1 5 10 15
 Ser Cys Cys Ser Leu Thr Gly Gly Gly Tyr Ala Ala Glu Ile Met Val
 20 25 30
 Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr
 35 40 45
 Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu
 50 55 60
 Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser
 65 70 75 80
 Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His
 85 90 95
 Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu
 100 105 110
 Ser Asp Ser Ala Asn Ser Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu
 115 120 125
 Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val Leu Pro Ala Ala
 130 135 140
 Thr Thr Asn Asn Gly Ser Gln Thr Pro Thr Thr Ser Thr Pro Ser
 145 150 155 160
 Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Asn Asn Glu
 165 170 175
 Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp Gly Gly Thr Ile
 180 185 190
 Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys Val Phe
 195 200 205
 Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr
 210 215 220
 Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Ile Ala Asn
 225 230 235 240
 Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val Gln Asp Gly Gln
 245 250 255

Gln	Gly	Val	Ser	Ser	Ser	Thr	Ser	Thr	Glu	Asp	Pro	Val	Val	Ser	Phe	
			260					265					270			
Ser	Arg	Asn	Thr	Ala	Val	Glu	Phe	Asp	Gly	Asn	Val	Ala	Arg	Val	Gly	
		275					280					285				
Gly	Gly	Ile	Tyr	Ser	Tyr	Gly	Asn	Val	Ala	Phe	Leu	Asn	Asn	Gly	Lys	
	290					295					300					
Thr	Leu	Phe	Leu	Asn	Asn	Val	Ala	Ser	Pro	Val	Tyr	Ile	Ala	Ala	Glu	
305					310					315					320	
Gln	Pro	Thr	Asn	Gly	Gln	Ala	Ser	Asn	Thr	Ser	Asp	Asn	Tyr	Gly	Asp	
			325						330						335	
Gly	Gly	Ala	Ile	Phe	Cys	Lys	Asn	Gly	Ala	Gln	Ala	Ala	Gly	Ser	Asn	
		340						345					350			
Asn	Ser	Gly	Ser	Val	Ser	Phe	Asp	Gly	Glu	Gly	Val	Val	Phe	Phe	Ser	
		355					360					365				
Ser	Asn	Val	Ala	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ala	Lys	Lys	Leu	
	370					375					380					
Ser	Val	Ala	Asn	Cys	Gly	Pro	Val	Gln	Phe	Leu	Gly	Asn	Ile	Ala	Asn	
385					390					395					400	
Asp	Gly	Gly	Ala	Ile	Tyr	Leu	Gly	Glu	Ser	Gly	Glu	Leu	Ser	Leu	Ser	
			405					410						415		
Ala	Asp	Tyr	Gly	Asp	Ile	Ile	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Thr	Ala	
		420						425					430			
Lys	Glu	Asn	Ala	Ala	Asp	Val	Asn	Gly	Val	Thr	Val	Ser	Ser	Gln	Ala	
		435					440					445				
Ile	Ser	Met	Gly	Ser	Gly	Gly	Lys	Ile	Thr	Thr	Leu	Arg	Ala	Lys	Ala	
	450				455						460					
Gly	His	Gln	Ile	Leu	Phe	Asn	Asp	Pro	Ile	Glu	Met	Ala	Asn	Gly	Asn	
465				470						475					480	
Asn	Gln	Pro	Ala	Gln	Ser	Ser	Glu	Pro	Leu	Lys	Ile	Asn	Asp	Gly	Glu	
			485						490					495		
Gly	Tyr	Thr	Gly	Asp	Ile	Val	Phe	Ala	Asn	Gly	Asn	Ser	Thr	Leu	Tyr	
		500					505						510			
Gln	Asn	Val	Thr	Ile	Glu	Gln	Gly	Arg	Ile	Val	Leu	Arg	Glu	Lys	Ala	
	515						520					525				
Lys	Leu	Ser	Val	Asn	Ser	Leu	Ser	Gln	Thr	Gly	Gly	Ser	Leu	Tyr	Met	
	530				535						540					
Glu	Ala	Gly	Ser	Thr	Leu	Asp	Phe	Val	Thr	Pro	Gln	Pro	Pro	Gln	Gln	
545					550					555					560	
Pro	Pro	Ala	Ala	Asn	Gln	Leu	Ile	Thr	Leu	Ser	Asn	Leu	His	Leu	Ser	
			565						570					575		
Leu	Ser	Ser	Leu	Leu	Ala	Asn	Asn	Ala	Val	Thr	Asn	Pro	Pro	Thr	Asn	
		580						585					590			
Pro	Pro	Ala	Gln	Asp	Ser	His	Pro	Ala	Val	Ile	Gly	Ser	Thr	Thr	Ala	
		595					600					605				
Gly	Pro	Val	Thr	Ile	Ser	Gly	Pro	Phe	Phe	Phe	Glu	Asp	Leu	Asp	Asp	
	610					615					620					
Thr	Ala	Tyr	Asp	Arg	Tyr	Asp	Trp	Leu	Gly	Ser	Asn	Gln	Lys	Ile	Asp	
625					630					635					640	
Val	Leu	Lys	Leu	Gln	Leu	Gly	Thr	Gln	Pro	Ser	Ala	Asn	Ala	Pro	Ser	
			645						650					655		
Asp	Leu	Thr	Leu	Gly	Asn	Glu	Met	Pro	Lys	Tyr	Gly	Tyr	Gln	Gly	Ser	
		660						665					670			
Trp	Lys	Leu	Ala	Trp	Asp	Pro	Asn	Thr	Ala	Asn	Asn	Gly	Pro	Tyr	Thr	
		675					680					685				
Leu	Lys	Ala	Thr	Trp	Thr	Lys	Thr	Gly	Tyr	Asn	Pro	Gly	Pro	Glu	Arg	
	690					695					700					
Val	Ala	Ser	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Ile	Leu	Asp	Ile	
705					710					715					720	
Arg	Ser	Ala	His	Ser	Ala	Ile	Gln	Ala	Ser	Val	Asp	Gly	Arg	Ser	Tyr	
			725						730					735		
Cys	Arg	Gly	Leu	Trp	Val	Ser	Gly	Val	Ser	Asn	Phe	Ser	Tyr	His	Asp	
			740					745					750			

Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser
 755 760 765
 Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala Phe
 770 775 780
 Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn
 785 790 795 800
 His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Lys Gln Ala Leu
 805 810 815
 Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly
 820 825 830
 Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Ser
 835 840 845
 Asp Val Arg Trp Asp Asn Asn Cys Leu Val Gly Glu Ile Gly Val Gly
 850 855 860
 Leu Pro Ile Val Thr Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg
 865 870 875 880
 Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr
 885 890 895
 Glu Glu Gly Asp Gln Ala Arg Ala Phe Arg Ser Gly His Leu Met Asn
 900 905 910
 Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His
 915 920 925
 Pro Asn Lys Tyr Ser Phe Met Gly Ala Tyr Ile Cys Asp Ala Tyr Arg
 930 935 940
 Thr Ile Ser Gly Thr Gln Thr Thr Leu Leu Ser His Gln Glu Thr Trp
 945 950 955 960
 Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Ile Val Arg Gly
 965 970 975
 Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly
 980 985 990
 Arg Tyr Glu Tyr Arg Asp Thr Ser Arg Gly Tyr Gly Leu Ser Ala Gly
 995 1000 1005
 Ser Lys Val Arg Phe
 1010

<210> 17
 <211> 505
 <212> PRT
 <213> Chlamydia sp.

<400> 17
 Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val
 1 5 10 15
 Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe
 20 25 30
 Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala
 35 40 45
 Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu
 50 55 60
 Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn
 65 70 75 80
 Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu
 85 90 95
 Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val
 100 105 110
 Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Thr
 115 120 125
 Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu
 130 135 140
 Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp
 145 150 155 160

Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys
 165 170 175
 Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys
 180 185 190
 Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala
 195 200 205
 Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val
 210 215 220
 Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro
 225 230 235 240
 Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val
 245 250 255
 Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu
 260 265 270
 Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr
 275 280 285
 Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn
 290 295 300
 Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala
 305 310 315 320
 Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val
 325 330 335
 Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala
 340 345 350
 Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu Arg Asn
 355 360 365
 Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu
 370 375 380
 Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys
 385 390 395 400
 Arg Thr Ala Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser
 405 410 415
 Ser Gln Ala Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg
 420 425 430
 Ala Lys Ala Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala
 435 440 445
 Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys Ile Asn
 450 455 460
 Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Ser Ser
 465 470 475 480
 Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg
 485 490 495
 Glu Lys Ala Lys Leu Ser Val Asn Ser
 500 505

<210> 18
 <211> 57
 <212> DNA
 <213> Chlamydia sp.

<400> 18
 aagggcccaa ttacgcagag ctcgagagaa attatgggttc ctcaaggaat ttacgat

57

<210> 19
 <211> 20
 <212> DNA
 <213> Chlamydia sp.

<400> 19
 cgctctagaa ctagtgatc

20

<210> 20

<211> 22
 <212> DNA
 <213> Chlamydia sp.

<400> 20
 atggttcctc aaggaattta cg

22

<210> 21
 <211> 19
 <212> DNA
 <213> Chlamydia sp.

<400> 21
 ggtcccccat cagcgggag

19

<210> 22
 <211> 1515
 <212> DNA
 <213> Chlamydia sp.

<400> 22
 gaaatcatgg ttcctcaagg aatttacgat ggggagacgt taactgtatc atttccctat 60
 actggttatag gagatccgag tgggactact gttttttctg caggagagtt aacattaaaa 120
 aatccttgaca attctattgc agctttgcct ttaagttggt ttgggaactt attagggagt 180
 tttactgttt tagggagagg acactcggtg actttcgaga acatacggac ttctacaaat 240
 ggggcagctc taagtaatag cgctgctgat ggactgttta ctattgaggg ttttaaagaa 300
 ttatcctttt ccaattgcaa ttcattactt gccgtactgc ctgctgcaac gactaataag 360
 ggtagccaga ctccgacgac aacatctaca ccgtctaatt gtactattta ttctaaaaca 420
 gatcttttgt tactcaataa tgagaagttc tcattctata gtaatttagt ctctggagat 480
 gggggagcta tagatgctaa gagcttaacg gttcaaggaa ttagcaagct ttgtgtcttc 540
 caagaaaata ctgctcaagc tgatggggga gcttgtcaag tagtcaccag tttctctgct 600
 atggctaacg aggcctcctat tgcctttgta gcgaatgttg caggagtaag agggggaggg 660
 attgctgctg ttcaggatgg gcagcaggga gtgtcatcat ctacttcaac agaagatcca 720
 gtagtaagtt tttccagaaa tactgcggta gagtttgatg ggaacgtagc ccgagtagga 780
 ggaggggattt actcctacgg gaacgttgct ttctgaata atggaaaaac cttgtttctc 840
 aacaatgttg cttctcctgt ttacattgct gctaagcaac caacaagtgg acaggcttct 900
 aatacgagta ataattacgg agatggagga gctatcttct gtaagaatgg tgcgcaagca 960
 ggatccaata actctggatc agtttccctt gatggagagg gagtagtttt ctttagtagc 1020
 aatgtagctg ctgggaaagg gggagctatt tatgccaaaa agctctcggt tgctaactgt 1080
 ggccctgtac aatttttaag gaatatcgct aatgatggtg gagcgattta tttaggagaa 1140
 tctggagagc tcagttttatc tgctgattat ggagatatta ttttcgatgg gaatcttaaa 1200
 agaacagcca aagagaatgc tgccgatgtt aatggcgtaa ctgtgtcctc acaagccatt 1260
 tcgatgggat cgggagggaa aataacgaca ttaagagcta aagcagggca tcagattctc 1320
 tttaatgata ccactcgagat ggcaaacgga aataaccagc cagcgcagtc ttccaaactt 1380
 ctaaaaatta acgatggtga aggatacaca ggggatattg tttttgctaa tggaagcagt 1440
 actttgtacc aaaatgttac gatagagcaa ggaaggattg ttcttcgtga aaaggcaaaa 1500
 ttatcagtga attct 1515

<210> 23
 <211> 3354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Recombinant Expression Vector

<400> 23
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 ttaactgtat catttcccta tactgttata ggagatccga gtgggactac tgttttttct 180
 gcaggagagt taacgttaaa aaatcttgac aattctattg cagctttgcc ttttaagttg 240
 tttgggaact tattagggag ttttactggt ttagggagag gacactcgtt gactttcgag 300

aacatacggg	cttctacaaa	tggagctgca	ctaagtgaca	gcgctaatag	cgggttattt	360
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cctgctgcaa	cgactaataa	tggtagccag	actccgctga	caacatctac	accgtctaatt	480
ggtactattt	attctaaaaa	agatcttttg	ttactcaata	atgagaagtt	ctcatttctat	540
agtaattcag	tctctggaga	tgggggagct	atagatgcta	agagcttaac	ggttcaaggga	600
attagcaagc	tttgtgtott	ccaagaaaat	actgctcaag	ctgatggggg	agcttgtcaa	660
gtagtcacca	gtttctctgc	tatggctaac	gaggctccta	ttgcctttgt	agcgaatggt	720
gcaggagtaa	gagggggagg	gattgctgct	gttcaggatg	ggcagcaggg	agtgtcatca	780
tctacttcaa	cagaagatcc	agtagtaagt	ttttccagaa	atactgcggt	agagtttgat	840
gggaacgtag	cccagtagtg	aggagggatt	tactcctacg	ggaacgttgc	tttcttgaat	900
aatggaaaaa	ccttgtttct	caacaatggt	gcttctcctg	tttacattgc	tgctgagcaa	960
ccaacaaatg	gacaggcttc	taatacagag	gataattacg	gagatggagg	agctatcttc	1020
tgtaagaatg	gtgcgcaagc	agcaggatcc	aataactctg	gatcagtttc	ctttgatgga	1080
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cctgagcgag	tgccttcttt	ggttccaaat	agtttatggg	gatccatttt	agataacga	2160
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tttaaggggg	acgatgttta	cttgaatgga	gactgcgctt	ttgtcaatgt	ctatgcaggg	3240
gcagagaacg	gctcaattat	ctcagctaag	ggcgacaatt	taacgattac	cggacaaaac	3300
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<210> 24

<211> 3324

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant Expression Vector

<400> 24

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acgttaactg	tatcattttcc	ctatactggt	ataggagatc	cgagtgggac	tactgttttt	180
tctgcaggag	agttaacgtt	aaaaaatctt	gacaattcta	ttgcagcttt	gcctttaagt	240
tgttttggga	acttattagg	gagttttact	gttttaggga	gaggacactc	gttgactttc	300
gagaacatac	ggacttctac	aaatggagct	gcactaagtg	acagcgctaa	tagcgggtta	360
tttactattg	agggttttaa	agaattatct	ttttccaatt	gcaactcatt	acttgccgta	420
ctgcoctgctg	caacgactaa	taatggtagc	cagactccga	cgacaacatc	tacaccgtct	480
aatgggtacta	tttatttctaa	aacagatcct	ttgttactca	ataatgagaa	gttctcattc	540
tatagtaatt	tagtctctgg	agatggggga	actatagatg	ctaagagctt	aacggttcaa	600
ggaattagca	agctttgtgt	cttccaagaa	aatactgctc	aagctgatgg	gggagcttgt	660
caagtagtca	ccagtttctc	tgctatggct	aacgaggctc	ctattgcctt	tatagcgaat	720
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aaccatgcat	tatcattttac	agat				3324

<210> 25
 <211> 65
 <212> PRT
 <213> Chlamydia sp.

<400> 25
 Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala
 1 5 10 15
 Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Pro Leu
 20 25 30
 Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly
 35 40 45
 His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala
 50 55 60
 Leu

65
 <210> 26
 <211> 24
 <212> PRT
 <213> Chlamydia sp.

<400> 26
 Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu His Leu Ser Leu Ser
 1 5 10 15
 Ser Leu Leu Ala Asn Asn Ala Val
 20

<210> 27
 <211> 8
 <212> PRT
 <213> Chlamydia sp.

<400> 27
 Gly Tyr Thr Gly Asp Ile Val Phe
 1 5
 <210> 28
 <211> 7
 <212> PRT
 <213> Chlamydia sp.

<400> 28
 Tyr Gly Asp Ile Ile Phe Asp
 1 5
 <210> 29
 <211> 63
 <212> PRT
 <213> Chlamydia sp.

<400> 29
 Gly Tyr Ala Ala Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu
 1 5 10 15
 Thr Leu Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly
 20 25 30
 Thr Thr Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn
 35 40 45
 Ser Ile Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly
 50 55 60

<210> 30
 <211> 22
 <212> PRT
 <213> Chlamydia sp.

<400> 30
 Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys
 1 5 10 15
 Ile Asn Asp Gly Glu Gly
 20

<210> 31

<211> 14
<212> PRT
<213> Chlamydia sp.

<400> 31
Ala Asn Gly Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu
1 5 10
<210> 32
<211> 10
<212> PRT
<213> Chlamydia sp.

<400> 32
Lys Leu Ser Val Asn Ser Leu Ser Gln Thr
1 5 10
<210> 33
<211> 45
<212> PRT
<213> Chlamydia sp.

<400> 33
Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile
1 5 10 15
Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu
20 25 30
Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu
35 40 45
<210> 34
<211> 64
<212> PRT
<213> Chlamydia sp.

<400> 34
Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile
1 5 10 15
Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu
20 25 30
Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly Thr Lys
35 40 45
Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu Met Pro
50 55 60
<210> 35
<211> 10
<212> PRT
<213> Chlamydia sp.

<400> 35
Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr
1 5 10
<210> 36
<211> 458
<212> PRT
<213> Chlamydia sp.

<400> 36
Gly Gly Ala Cys Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu
1 5 10 15
Ala Pro Ile Ala Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly
20 25 30
Ile Ala Ala Val Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser
35 40 45
Thr Glu Asp Pro Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe

50	55	60
Asp Gly Asn Val Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn		
65	70	75
Val Ala Phe Leu Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala		
85	90	95
Ser Pro Val Tyr Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser		
100	105	110
Asn Thr Ser Asn Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn		
115	120	125
Gly Ala Gln Ala Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly		
130	135	140
Glu Gly Val Val Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly		
145	150	155
Ala Ile Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln		
165	170	175
Phe Leu Arg Asn Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu		
180	185	190
Ser Gly Glu Leu Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp		
195	200	205
Gly Asn Leu Lys Arg Thr Ala Lys Glu Asn Ala Ala Asp Val Asn Gly		
210	215	220
Val Thr Val Ser Ser Gln Ala Ile Ser Met Gly Ser Gly Gly Lys Ile		
225	230	235
Thr Thr Leu Arg Ala Lys Ala Gly His Gln Ile Leu Phe Asn Asp Pro		
245	250	255
Ile Glu Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu		
260	265	270
Leu Lys Ile Asn Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala		
275	280	285
Asn Gly Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg		
290	295	300
Ile Val Leu Arg Glu Lys Ala Lys Leu Ser Val Asn Ser Leu Ser Gln		
305	310	315
Thr Gly Gly Ser Leu Tyr Met Glu Ala Gly Ser Thr Trp Asp Phe Val		
325	330	335
Thr Pro Gln Pro Pro Gln Gln Pro Pro Ala Ala Asn Gln Leu Ile Thr		
340	345	350
Leu Ser Asn Leu His Leu Ser Leu Ser Ser Leu Leu Ala Asn Asn Ala		
355	360	365
Val Thr Asn Pro Pro Thr Asn Pro Pro Ala Gln Asp Ser His Pro Ala		
370	375	380
Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile		
385	390	395
Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu		
405	410	415
Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly Thr Lys		
420	425	430
Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu Met Pro		
435	440	445
Lys Tyr Gly Tyr Gln Gly Ser Trp Lys Leu		
450	455	

<210> 37
 <211> 325
 <212> PRT
 <213> Chlamydia sp.

<400> 37
 Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu Arg
 1 5 10 15
 Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp Ile
 20 25 30
 Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser Tyr

	35		40		45										
Cys	Arg	Gly	Leu	Trp	Val	Ser	Gly	Val	Ser	Asn	Phe	Phe	Tyr	His	Asp
50						55					60				
Arg	Asp	Ala	Leu	Gly	Gln	Gly	Tyr	Arg	Tyr	Ile	Ser	Gly	Gly	Tyr	Ser
65					70					75					80
Leu	Gly	Ala	Asn	Ser	Tyr	Phe	Gly	Ser	Ser	Met	Phe	Gly	Leu	Ala	Phe
			85						90					95	
Thr	Glu	Val	Phe	Gly	Arg	Ser	Lys	Asp	Tyr	Val	Val	Cys	Arg	Ser	Asn
			100					105					110		
His	His	Ala	Cys	Ile	Gly	Ser	Val	Tyr	Leu	Ser	Thr	Gln	Gln	Ala	Leu
		115					120					125			
Cys	Gly	Ser	Tyr	Leu	Phe	Gly	Asp	Ala	Phe	Ile	Arg	Ala	Ser	Tyr	Gly
130						135					140				
Phe	Gly	Asn	Gln	His	Met	Lys	Thr	Ser	Tyr	Thr	Phe	Ala	Glu	Glu	Ser
145					150					155					160
Asp	Val	Arg	Trp	Asp	Asn	Asn	Cys	Leu	Ala	Gly	Glu	Ile	Gly	Ala	Gly
			165						170					175	
Leu	Pro	Ile	Val	Ile	Thr	Pro	Ser	Lys	Leu	Tyr	Leu	Asn	Glu	Leu	Arg
			180					185					190		
Pro	Phe	Val	Gln	Ala	Glu	Phe	Ser	Tyr	Ala	Asp	His	Glu	Ser	Phe	Thr
		195					200					205			
Glu	Glu	Gly	Asp	Gln	Ala	Arg	Ala	Phe	Lys	Ser	Gly	His	Leu	Leu	Asn
210						215					220				
Leu	Ser	Val	Pro	Val	Gly	Val	Lys	Phe	Asp	Arg	Cys	Ser	Ser	Thr	His
225					230					235					240
Pro	Asn	Lys	Tyr	Ser	Phe	Met	Ala	Ala	Tyr	Ile	Cys	Asp	Ala	Tyr	Arg
			245						250					255	
Thr	Ile	Ser	Gly	Thr	Glu	Thr	Thr	Leu	Leu	Ser	His	Gln	Glu	Thr	Trp
			260					265					270		
Thr	Thr	Asp	Ala	Phe	His	Leu	Ala	Arg	His	Gly	Val	Val	Val	Arg	Gly
		275					280					285			
Ser	Met	Tyr	Ala	Ser	Leu	Thr	Ser	Asn	Ile	Glu	Val	Tyr	Gly	His	Gly
290						295				300					
Arg	Tyr	Glu	Tyr	Arg	Asp	Ala	Ser	Arg	Gly	Tyr	Gly	Leu	Ser	Ala	Gly
305					310					315					320
Ser	Arg	Val	Arg	Phe											
				325											

<210> 38
 <211> 0
 <212> DNA
 <213> Chlamydia sp.

<400> 38
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3

<210> 39
 <211> 0
 <212> DNA
 <213> Chlamydia sp.

<400> 39
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<210> 40
 <211> 0
 <212> DNA
 <213> Chlamydia sp.

<400> 40
 000
 <210> 41
 <211> 0

<212> DNA
 <213> Chlamydia sp.

<400> 41
 000
 <210> 42
 <211> 6
 <212> PRT
 <213> Chlamydia sp.

<400> 42
 Glu Ile Met Val Pro Gln
 1 5
 <210> 43
 <211> 984
 <212> PRT
 <213> Chlamydia sp.

<400> 43
 Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val
 1 5 10 15
 Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe
 20 25 30
 Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala
 35 40 45
 Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu
 50 55 60
 Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn
 65 70 75 80
 Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu
 85 90 95
 Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val
 100 105 110
 Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Thr
 115 120 125
 Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu
 130 135 140
 Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp
 145 150 155 160
 Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys
 165 170 175
 Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys
 180 185 190
 Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala
 195 200 205
 Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val
 210 215 220
 Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro
 225 230 235 240
 Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val
 245 250 255
 Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu
 260 265 270
 Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr
 275 280 285
 Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn
 290 295 300
 Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala
 305 310 315 320
 Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val
 325 330 335
 Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala

		835					840				845			
Glu	Leu	Arg	Pro	Phe	Val	Gln	Ala	Glu	Phe	Ser	Tyr	Ala	Asp	His
	850					855					860			
Ser	Phe	Thr	Glu	Glu	Gly	Asp	Gln	Ala	Arg	Ala	Phe	Lys	Ser	Gly
865					870					875				880
Leu	Leu	Asn	Leu	Ser	Val	Pro	Val	Gly	Val	Lys	Phe	Asp	Arg	Cys
				885					890					895
Ser	Thr	His	Pro	Asn	Lys	Tyr	Ser	Phe	Met	Ala	Ala	Tyr	Ile	Cys
			900					905					910	Asp
Ala	Tyr	Arg	Thr	Ile	Ser	Gly	Thr	Glu	Thr	Thr	Leu	Leu	Ser	His
			915					920					925	Gln
Glu	Thr	Trp	Thr	Thr	Asp	Ala	Phe	His	Leu	Ala	Arg	His	Gly	Val
	930					935								Val
Val	Arg	Gly	Ser	Met	Tyr	Ala	Ser	Leu	Thr	Ser	Asn	Ile	Glu	Val
945					950					955				Tyr
Gly	His	Gly	Arg	Tyr	Glu	Tyr	Arg	Asp	Ala	Ser	Arg	Gly	Tyr	Gly
				965					970					Leu
Ser	Ala	Gly	Ser	Arg	Val	Arg	Phe							975
			980											